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Raw Sequence Listing Error Summary

#4

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/434,708

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|---------------------------------------|---|
| 1 | ____ Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | ____ Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | ____ Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | ____ Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | ____ Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | ____ Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 | ____ PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. |
| 8 | ____ Skipped Sequences (OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | ____ Skipped Sequences (NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 10 | ____ Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 | ____ Use of <213>Organism (NEW RULES) | Sequence(s) ____ are missing this mandatory field or its response. |
| 12 | ____ Use of <220>Feature (NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | ____ PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |

PAGE : 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/434,708

DATE: 11/18/1999
TIME: 14:43:39

Input Set: I434708.RAW

This Raw Listing contains the General Information Section and up to first 5 pages. Does Not C

Information Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Borriello, Francescopaolo
2 Band, Hamid
3 <120> TITLE OF INVENTION: Characterization of a novel gene Cbl-SL
4 <130> FILE REFERENCE: B0801/7159/ERP
5 <140> CURRENT APPLICATION NUMBER: US/09/434,708
6 <141> CURRENT FILING DATE: 1999-11-05
7 <150> EARLIER APPLICATION NUMBER: U.S. 60/107,470
8 <151> EARLIER FILING DATE: 1998-11-06
9 <160> NUMBER OF SEQ ID NOS: 10
10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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18 <400> SEQUENCE: 1
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21 1 5 10
22 gag gcc cgc gcc ctg ggc cgg gca gtc agg atg ctg cag cgc cta gaa 99
23 Glu Ala Arg Ala Leu Gly Arg Ala Val Arg Met Leu Gln Arg Leu Glu
24 15 20 25
25 gag caa tgc gtc gac ccc cgg ctg tcc gtg agt ccc cct tcg ctg cgg 147
26 Glu Gln Cys Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg
27 30 35 40 45
28 gac ctg ctg ccc cgc aca gcg cag ctg ctt cga gag gtg gcc cat tct 195
29 Asp Leu Leu Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser
30 50 55 60
31 cgg cgg ggc ggc gga ggc ggc ccc ggg ggt ccc ggc ggc tct ggg 243
32 Arg Arg Ala Ala Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly
33 65 70 75
34 gac ttt cta ctc atc tac ctg gcc aat ctg gag gcc aag agc agg cag 291
35 Asp Phe Leu Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln
36 80 85 90
37 gtg gcc gcg ctg ctg cct ccc cgg ggc cga agg agt gcc aac gac gag 339
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39 95 100 105
40 ctc ttc cgg ggc tcc aga ctc agg cga cag ctg gcc aag ctg gcc 387
41 Leu Phe Arg Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala
42 110 115 120 125
43 atc atc ttc agc cac atg cac gca gag ctg cac gca ctc ttc ccc ggg 435
44 Ile Ile Phe Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly

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RAW SEQUENCE LISTING
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DATE: 11/18/1999
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Input Set: I434708.RAW

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48	acc ttc tgg agg gaa agt tgc gga gcc cggttgtgtctgtccc tgg gct			531
49	Thr Phe Trp Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala			
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51	gag ttt gag tcc ctc ctg ggc acc tgc cac cct gtg gaa cca ggc tgc			579
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53	175	180	185	
54	aca gcc ctg gcc ttg cgc acc acc att gac ctc acc tgc agc ggg cac			627
55	Thr Ala Leu Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His			
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57	gtg tcc atc ttc gag ttc gac gtc ttc acc agg ctc ttt cag cca tgg			675
58	Val Ser Ile Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp			
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60	cca aca ctc ctc aag aac tgg cag ctc ctg gca gtc aac cac cca ggc			723
61	Pro Thr Leu Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly			
62	225	230	235	
63	tac atg gcc ttc ctc acc tat gat gag gtc caa gag cgt ctg cag gcc			771
64	Tyr Met Ala Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala			
65	240	245	250	
66	tgc agg gac aag cca ggc agt tac atc ttc cgg ccc agc tgt act cgc			819
67	Cys Arg Asp Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg			
68	255	260	265	
69	ctg ggg cag tgg gcc atc ggc tat gtg agc tca gat ggc agc atc ctg			867
70	Leu Gly Gln Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu			
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72	cag acc atc cct gcc aac aaa ccc ctg tcc cag gtg ctc ctg gag gga			915
73	Gln Thr Ile Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Glu Gly			
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76	Gln Lys Asp Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro			
77	305	310	315	
78	gac ctg act gag ctc ggc cag gca gaa ccc cag cag cgc atc cac gtg			1011
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81	tca gag gag cag ctg cag ctc tac tgg gcc atg gac tcc aca ttt gag			1059
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84	ctc tgc aag atc tgt gct gag agc aac aag gat gtg aag att gag ccg			1107
85	Leu Cys Lys Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro			
86	350	355	360	365
87	tgc ggg cac ctg ctc tgc agc tgc tgc ctg gct gcc tgg cag cac tcg			1155
88	Cys Gly His Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser			
89	370	375	380	
90	gac agc cag acc tgc ccc ttc tgc cgc tgc gag atc aag ggc tgg gag			1203
91	Asp Ser Gln Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu			
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93	gcc gtg agt atc tac cag ttc cac ggt cag gct act gct gag gac tca			1251

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/434,708DATE: 11/18/1999
TIME: 14:43:39

Input Set: I434708.RAW

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 97 ggg aac agc agt gac cag gaa ggc agg gag ttg gag ctg ggg cag gtg 1299
 98 Gly Asn Ser Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val
 99 415 420 425
 100 ccc ctt tcg gct cct cca ttg ccc cca cgg cca gat ctg ccc ccc agg 1347
 101 Pro Leu Ser Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg
 102 430 435 440 445
 103 aag ccc aga aat gcc cag ccg aaa gtg aga ctc cta aag ggg aac tcc 1395
 104 Lys Pro Arg Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser
 105 450 455 460
 106 cct cca gct gcg ctg gga ccc cag gac cct gcc ccg gcc tgaaggccag 1444
 107 Pro Pro Ala Ala Leu Gly Pro Gln Asp Pro Ala Pro Ala
 108 465 470
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 113 <212> TYPE: PRT
 114 <213> ORGANISM: Homo Sapiens
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 120 Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg Asp Leu Leu
 121 35 40 45
 122 Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser Arg Arg Ala
 123 50 55 60
 124 Ala Gly Gly Gly Pro Gly Gly Pro Gly Ser Gly Asp Phe Leu
 125 65 70 75 80
 126 Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln Val Ala Ala
 127 85 90 95
 128 Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu Leu Phe Arg
 129 100 105 110
 130 Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala Ile Ile Phe
 131 115 120 125
 132 Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly Ala Lys Tyr
 133 130 135 140
 134 Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His Thr Phe Trp
 135 145 150 155 160
 136 Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala Glu Phe Glu
 137 165 170 175
 138 Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys Thr Ala Leu
 139 180 185 190
 140 Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His Val Ser Ile
 141 195 200 205
 142 Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp Pro Thr Leu
 143 210 215 220
 144 Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly Tyr Met Ala

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RAW SEQUENCE LISTING
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Input Set: I434708.RAW

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150	Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser	Ile Leu Gln Thr Ile		
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152	Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu	Glu Gly Gln Lys Asp		
153	290	295	300	
154	Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His	Asn Pro Asp Leu Thr		
155	305	310	315	320
156	Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg	Ile His Val Ser Glu Glu		
157	325	330	335	
158	Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr	Phe Glu Leu Cys Lys		
159	340	345	350	
160	Ile Cys Ala Glu Ser Asn Lys Asp Val Lys	Ile Glu Pro Cys Gly His		
161	355	360	365	
162	Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp	Gln His Ser Asp Ser Gln		
163	370	375	380	
164	Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys	Gly Trp Glu Ala Val Ser		
165	385	390	395	400
166	Ile Tyr Gln Phe His Gly Gln Ala Thr Ala	Glu Asp Ser Gly Asn Ser		
167	405	410	415	
168	Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu	Gly Gln Val Pro Leu Ser		
169	420	425	430	
170	Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu	Pro Pro Arg Lys Pro Arg		
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172	Asn Ala Gln Pro Lys Val Arg Leu Leu Lys	Gly Asn Ser Pro Pro Ala		
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183	cccccttcgc tgcgggacct gctgccccgc acagcgcagc	tgcttcgaga gttggcccat	180	
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192	tggccaaacac tcctcaagaa ctggcagctc ctggcagtca	accaccagg ctacatggcc	720	
193	ttcctcacct atgatgaggt ccaagagcgt ctgcaggcc	gcagggacaa gccaggcagt	780	
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W-->	241 <i>den</i> 10 → cctggcagaa ctcagacagn ccagacctgc cttttctgg cctgtccag attcaagggg	360
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VERIFICATION SUMMARY
PATENT APPLICATION US/09/434,708DATE: 11/18/1999
TIME: 14:43:39

Input Set: I434708.RAW

Line ? Error/Warning

Original Text

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243 W "N" or "Xaa" used: Feature required

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